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#3

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/759,207

DATE: 01/29/2001
TIME: 13:14:20

Input Set : A:\Seq.txt
Output Set: N:\CRF3\01292001\I759207.raw

ENTERED

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
C--> 4 (i) APPLICANT: Iris Pecker et al.
5 (ii) TITLE OF INVENTION: HEPARANASE SPECIFIC MOLECULAR PROBES
6 AND THEIR USE IN RESEARCH AND MEDICAL
7 APPLICATIONS
8 (iii) NUMBER OF SEQUENCES: 7
9 (iv) CORRESPONDENCE ADDRESS:
10 (A) ADDRESSEE: G. E. Ehrlich (1995) Ltd.
11 c/o Anthony Castorina
12 (B) STREET: 2001 Jefferson Davis Highway, Suite 207
13 (C) CITY: Arlington
14 (D) STATE: Virginia
15 (E) COUNTRY: United States of America
16 (F) ZIP: 22202
17 (v) COMPUTER READABLE FORM:
18 (A) MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
19 (B) COMPUTER: Twinhead* Slimnote-890TX
20 (C) OPERATING SYSTEM: MS DOS version 6.2,
21 Windows version 3.11
22 (D) SOFTWARE: Word for Windows version 2.0 converted to
23 an ASCII file
24 (vi) CURRENT APPLICATION DATA:
C--> 25 (A) APPLICATION NUMBER: US/09/759,207
C--> 26 (B) FILING DATE: 16-Jan-2001
27 (C) CLASSIFICATION:
28 (vii) PRIOR APPLICATION DATA:
29 (A) APPLICATION NUMBER: 08/922,180
30 (B) FILING DATE: September 2, 1997
31 (A) APPLICATION NUMBER: 09/071,739
32 (B) FILING DATE: May 1, 1998
33 (A) APPLICATION NUMBER: 09/322,977
34 (B) FILING DATE: June 1, 1999
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: Sol Sheinbein
37 (B) REGISTRATION NUMBER: 25,457
38 (C) REFERENCE/DOCKET NUMBER: 00/21505
39 (ix) TELECOMMUNICATION INFORMATION:
40 (A) TELEPHONE: 972-3-6127676
41 (B) TELEFAX: 972-3-6127575
42 (C) TELEX:
44 (2) INFORMATION FOR SEQ ID NO: 1:
45 (i) SEQUENCE CHARACTERISTICS:
46 (A) LENGTH: 1721
47 (B) TYPE: nucleic acid
48 (C) STRANDEDNESS: double
49 (D) TOPOLOGY: linear

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C--> 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 51 CTAGACCTTT CGACTCTCCG CTCCGCCGCA GCTGCCGGCA GGAGCAGCCA CGTGAGCCCA 60
 52 AGATGCTGCT GCGCTCGAAG CCTGCCGCTGC CGCCGCCGCT GATGCTGCTG CTCCCTGGGC 120
 53 CGC'GGGTCC CCTC'CCCTC GGCGCCCTGC CCCGACCTGC GCAAGCACAG GACGTCGTGC 180
 C--> 54 ACCTGGACTT CTTCACCCAG GAGCCGCTGC ACCTGGTGAG CCCCTCGTTC CTGTCGTCA 240
 55 CCATTGACCC CAACCTGGCC ACCGACCCCG CGTTCCTCAT CCTCCCTGGGT TC'TCAAAGC 300
 56 TTCG'TACCTT GGCAGAGGC TTGTCCTCTG CGTACCTGAG GTTGGGTGCG ACCAAGACAG 360
 57 ACTTCCTAAAT TTTCGATCCC AAGAAGGAAT CAACCTTTGA AGAGAGAAAGT TACTGGCAAT 420
 58 CTCAAAGTCAA CCACGATATT TGCAAATATG GATCCATCCC TCCTGATGTG GAGCAGAAGT 480
 59 TACGGTTGGA ATGGCCCTAC CAGGAGCAAT TGCTACTCCG AGAACACTAC CAGAAAAGT 540
 60 TCAAGAACAG CACCTACTCA AGAACGCTCG TAGATGTGCT ATACACTTTT GCAAACGTGCT 600
 61 CAGGACTGGA CTTGATCTT GGCCTAAATG CGTATTAAAG AACAGCAGAT TTCCAGTGGA 660
 62 ACAGCTCTAA TGCTCAGTTG CTCCCTGGACT ACTGCTCTTC CAAGGGGTAT AACATTTCTT 720
 63 GGGAACTAGG CAATGAACACT AACAGTTTC TTAAAGAAGGC TGATATTTC ATCAATGGGT 780
 64 CGCAGTTAGG AGAAGATTAT ATTCAATTGC ATAACCTTCT AAGAAAGTCC ACCTTCAAA 840
 65 ATGCAAAACT CTATGGCTCT GATGTTGGTC AGCCTCGAAG AAAGACGGCT AAGATGCTGA 900
 66 AGAGCTTCTT GAAGGCTGGT GGAGAAGTGA TTGATTCAGT TACATGGCAT CACTACTATT 960
 67 TGAATGGACG GACTGCTACC AGGGAAGATT TTCTAAACCC TGATGTATTG GACATTTTTA 1020
 68 TTTCATCTGT GCAAAAGATT TTCCAGGTGG TTGAGAGCAC CAGGCCTGGC AAGAAGGTCT 1080
 69 GGTTAGGAGA AACAAAGCTCT GCATATGGAG GCGGAGCGCC CTTGCTATCC GACACCTTTC 1140
 70 CAGCTGGCTT TATGTGGCTG GATAAATTGG GCCTGTCAGC CCGAATGGGA ATAGAAGTGG 1200
 71 TGATGAGGCA AGTATTCTTT GGAGCAGGAA ACTACCATTG AGTGGATGAA AACTTCGATC 1260
 72 CTTTACCTGA TTATTGGCTA TCTCTCTGT TCAAGAAATT GGTTGGCACC AAGGTGTTAA 1320
 73 TGGCAAGCGT GCAAGGCTCA AAGAGAAGGA AGCTTCGAGT ATACCTTCAT TGCACAAACA 1380
 74 CTGACAATCC AAGGTATAAA GAAGGAGATT TAACTCTGTA TGCCATAAAC CTCCATAACG 1440
 75 TCACCAAGTA CTTGCCGTTA CCCTATCCTT TTCTTAACAA GCAAGTGGAT AAATACCTTC 1500
 76 TAAGACCTTT GGGACCTCAT GGATTACTTT CCAAATCTGT CCAAACCTCAAT GGTCTAACTC 1560
 77 TAAAGATGGT GGATGATCAA ACCTTGCCAC CTTTAATGGG AAAACCTCTC CGGCCAGGAA 1620
 78 GTTCACTGGG CTTGCCAGCT TTCTCATATA GTTTTTCTG GATAAGAAAT GCCAAAGTTG 1680
 79 CTGCTTGAT CTGAAAATAA AATATACTAG TCCTGACACT G 1721
 81 (2) INFORMATION FOR SEQ ID NO: 2:
 82 (i) SEQUENCE CHARACTERISTICS:
 83 (A) LENGTH: 543
 84 (B) TYPE: amino acid
 85 (C) STRANDEDNESS: single
 86 (D) TOPOLOGY: linear
 C--> 87 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 88 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
 89 5 10 15
 90 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
 91 20 25 30
 92 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln-Glu Pro
 93 35 40 45
 94 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
 95 50 55 60
 96 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Gly Ser Pro Lys Leu
 97 65 70 75 80
 98 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
 99 85 90 95

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107 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Glu Ser Thr Phe
108 100 105 110
110 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
111 115 120 125
113 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
114 130 135 140
116 Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
117 145 150 155 160
119 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Val Leu Tyr Thr Phe
120 165 170 175
122 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
123 180 185 190
125 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
126 195 200 205
128 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
129 210 215 220
131 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
132 225 230 235 240
134 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
135 245 250 255
137 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
138 260 265 270
140 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
141 275 280 285
143 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
144 290 295 300
146 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
147 305 310 315 320
149 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
150 325 330 335
152 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala
153 340 345 350
155 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
156 355 360 365
158 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
159 370 375 380
161 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
162 385 390 395 400
164 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
165 405 410 415
167 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
168 420 425 430
170 Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly
171 435 440 445
173 Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu
174 450 455 460
176 Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu
177 465 470 475 480
179 Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn

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180 485 490 495
182 Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met
183 500 505 510
185 Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser
186 515 520 525
188 Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile
189 530 535 540 543

191 (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1721
- (B) TYPE: Nucleic acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

C--> 197 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

199	CT	AGA	GCT	TTC	GAC	14												
201	TCT	CCG	CTG	CGC	GGC	AGC	TGG	CGG	GGG	GAG	CAG	CCA	GGT	GAG	CCC	AAG	62	
203	ATG	CTG	CTG	CGC	TCG	AAG	CCT	CCG	CTG	CCG	CCG	CTG	ATG	CTG	CTG	CTG	110	
204	Met	Leu	Leu	Arg	Ser	Lys	Pro	Ala	Leu	Pro	Pro	Pro	Leu	Met	Leu	Leu		
205	5						10						15					
207	CTC	CTG	GGG	CCG	CTG	GGT	CCC	CTC	TCC	CCT	GGC	GCC	CTG	CCC	CGA	CCT	158	
208	Leu	Leu	Gly	Pro	Leu	Gly	Pro	Leu	Ser	Pro	Gly	Ala	Leu	Pro	Arg	Pro		
209	20						25						30					
211	GCG	CAA	GCA	CAG	GAC	GTC	GTG	GAC	CTG	GAC	TTC	TTC	ACC	CAG	GAG	CCG	206	
212	Ala	Gln	Ala	Gln	Asp	Val	Val	Asp	Leu	Asp	Phe	Phe	Thr	Gln	Glu	Pro		
213	35						40						45					
215	CTG	CAC	CTG	GTG	AGC	CCC	TCG	TTC	CTG	TCC	GTC	ACC	ATT	GAC	GCC	AAC	254	
216	Leu	His	Leu	Val	Ser	Pro	Ser	Phe	Leu	Ser	Val	Thr	Ile	Asp	Ala	Asn		
217	50						55						60					
219	CTG	GCC	ACG	GAC	CCG	CGG	TTC	TTC	CTC	ATC	CTC	CTG	GGT	TCT	CCA	AAG	CTT	302
220	Leu	Ala	Thr	Asp	Pro	Arg	Phe	Leu	Ile	Leu	Leu	Gly	Ser	Pro	Lys	Leu		
221	65						70						75			80		
223	CGT	ACC	TTG	GCC	AGA	GGC	TTG	TCT	CCT	CGC	TAC	CTG	AGG	TTT	GGT	GGC	350	
224	Arg	Thr	Leu	Ala	Arg	Gly	Leu	Ser	Pro	Ala	Tyr	Leu	Arg	Phe	Gly	Gly		
225	85						90						95					
227	ACC	AAG	ACA	GAC	TTC	CTA	ATT	TTC	GAT	CCC	AAG	AAG	GAA	TCA	ACC	TTT	398	
228	Thr	Lys	Thr	Asp	Phe	Leu	Ile	Phe	Asp	Pro	Lys	Lys	Glu	Ser	Thr	Phe		
229	100						105						110					
231	GAA	GAG	AGA	AGT	TAC	TGG	CAA	TCT	CAA	GTC	AAC	CAG	GAT	ATT	TGC	AAA	446	
232	Glu	Glu	Arg	Ser	Tyr	Trp	Gln	Ser	Gln	Val	Asn	Gln	Asp	Ile	Cys	Lys		
233	115						120						125					
235	TAT	GGA	TCC	ATC	CCT	CCT	GAT	GTG	GAG	GAG	AAG	TTA	CGG	TTG	GAA	TGG	494	
236	Tyr	Gly	Ser	Ile	Pro	Pro	Asp	Val	Glu	Glu	Lys	Ile	Arg	Leu	Glu	Trp		
237	130						135						140					
239	CCC	TAC	CAG	GAG	CAA	TTG	CTA	CTC	CGA	GAA	CAC	TAC	CAG	AAA	AAG	TTC	542	
240	Pro	Tyr	Gln	Glu	Gln	Leu	Leu	Arg	Glu	His	Tyr	Gln	Lys	Lys	Phe			
241	145						150						155			160		
243	AAG	AAC	AGC	ACC	TAC	TCA	AGA	AGC	TCT	GTA	GAT	GTG	CTA	TAC	ACT	TTT	590	
244	Lys	Asn	Ser	Thr	Tyr	Ser	Arg	Ser	Ser	Val	Asp	Val	Leu	Tyr	Thr	Phe		
245	165						170						175					

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247 GCA AAC TGC TCA GGA CTG GAC TTG ATC TTT GGC CTA AAT GCG TTA TTA 638
 248 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
 249 180 185 190
 251 AGA ACA GCA GAT TTG CAG TGG AAC ACT TCT AAT GCT CAG TTG CTC CTG 686
 252 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
 253 195 200 205
 255 GAC TAC TGC TCT TCC AAG GGG TAT AAC ATT TCT TTG GAA CTA GGC AAT 734
 256 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
 257 210 215 220
 259 GAA CCT AAC AGT TTC CTT AAG AAG GCT GAT ATT TTC ATC AAT GGG TCG 782
 260 Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser
 261 225 230 235 240
 263 CAG TTA GGA GAA GAT TAT ATT CAA TTG CAT AAA CTT CTA AGA AAG TCC 830
 264 Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser
 265 245 250 255
 267 ACC TTC AAA AAT GCA AAA CTC TAT GGT CCT GAT GTT GGT CAG CCT CGA 878
 268 Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg
 269 260 265 270
 271 AGA AAG ACG GCT AAG ATG CTG AAG AGC TTC CTG AAG GCT GGT GGA GAA 926
 272 Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu
 273 275 280 285
 275 GTG ATT GAT TCA GTT ACA TGG CAT CAC TAC TAT TTG AAT GGA CGG ACT 974
 276 Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr
 277 290 295 300
 279 GCT ACC AGG GAA GAT TTT CTA AAC CCT GAT GTC TTG GAC ATT TTT ATT 1022
 280 Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile
 281 305 310 315 320
 283 TCA TCT GTG CAA AAA GTT TTC CAG GTG GTT GAG AGC ACC AGG CCT GGC 1070
 284 Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly
 285 325 330 335
 287 AAG AAG GTC TCG TTA GGA GAA ACA AGC TCT GCA TAT GGA GGC GGA GCG 1118
 288 Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Ala
 289 340 345 350
 291 CCC TTG CTA TCC GAC ACC TTT GCA GCT GGC TTT ATG TGG CTG GAT AAA 1166
 292 Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys
 293 355 360 365
 295 TTG GGC CTG TCA GCC CGA ATG GGA ATA GAA GTG GTG ATG AGG CAA GTA 1214
 296 Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val
 297 370 375 380
 299 TTC TTT GGA GCA GGA AAC TAC CAT TTA GTG GAT GAA AAC TTC GAT CCT 1262
 300 Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro
 301 385 390 395 400
 303 TTA CCT GAT TAT TGG CTA TCT CTT CTG TTC AAG AAA TTG GTG GGC ACC 1310
 304 Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr
 305 405 410 415
 307 AAG GTG TTA ATG GCA AGC GTG CAA GGT TCA AAG AGA AGG AAG CCT CGA 1358
 308 Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg
 309 420 425 430
 311 GTA TAC CTT CAT TGC ACA AAC ACT GAC AAT CCA AGG TAT AAA GAA GGA 1406

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/759,207

DATE: 01/29/2001
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Input Set : A:\Seq.txt
Output Set: N:\CRF3\01292001\I759207.raw

L:4 M:220 C: Keyword misspelled or invalid format, [(i) APPLICANT:]
L:25 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:26 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:50 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:54 M:111 C: (47) String data converted to upper case,
L:87 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:197 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:347 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:356 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:365 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]
L:374 M:220 C: Keyword misspelled or invalid format, [(xi) SEQUENCE DESCRIPTION: SEQ ID NO:]